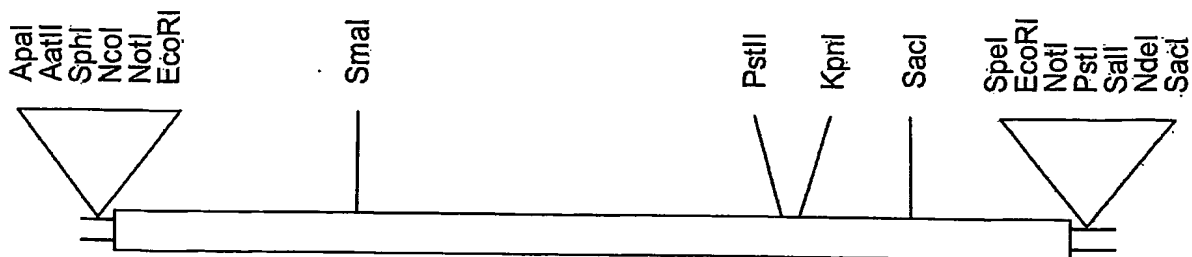


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TrCHSa3

FIGURE 1

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1 GAATTCAC TA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAAC
51 AAAAACAAC T ACGCATATTA TATATATATA TATATAGTCT ATAATTGAAA
101 GAAACTGCTA AAGATATTAT TAAGATATGG TGAGTGTAGC TGAAATTCGC
151 AAGGCTCAGA GGGCTGAAGG CCCTGCAACC ATTTTGGCCA TTGGCACTGC
201 AAATCCACCA AACCGTGTTG AGCAGAGCAC ATATCCTGAT TTCTACTTCA
251 AAATTACAAA CAGTGAGCAC AAGACTGAGC TCAAAGAGAA GTTCCAACGC
301 ATGTGTGACA AATCCATGAT CAAGAGCAGA TACATGTATC TAACAGAAGA
351 GATTTTGAAA GAAAATCCTA GTCTTTGTGA ATACATGGCA CCTTCATTGG
401 ATGCTAGGCA AGACATGGTG GTGGTTGAGG TACCTAGACT TGGGAAGGAG
451 GCTGCAGTCA AGGCCATTAA AGAATGGGGT CAACCAAAGT CAAAGATTAC
501 TCACTTAATC TTTTGCACCA CAAGTGGTGT TGACATGCCT GGTGCTGATT
551 ACCAACTCAC AAAACTCTTA GGTCTTCGCC CATATGTGAA AAGGTATATG
601 ATGTACCAAC AAGGTTGTTT TGCAGGAGGC ACGGTGCTTC GTTTGGCAAA
651 AGATTTGGCC GAGAACAACA AAGGTGCTCG TGTGCTAGTT GTTTGTTCGT
701 AAGTCACCGC AGTCACATTT CGCGGCCCCA GTGATACTCA CTTGGACAGT
751 CTTGTTGGAC AAGCATTGTT TGGAGATGGA GCCGCTGCAC TAATTGTTGG
801 TTCTGATCCA GTGCCTGAAA TTGAGAAACC AATATTTGAG ATGGTTTGA
851 CTGCACAAAC AATTGCTCCA GACAGTGAAG GTGCCATTGA TGGTCATCTT
901 CGTGAAGCTG GGCTAACATT TCATCTTCTT AAAGATGTTC CTGGGATTGT
951 ATCAAAGAAC ATTAATAAAG CATTGGTTGA GGCTTTCCAA CCATTAGGAA
1001 TTTCTGACTA CAACTCAATC TTTTGGATTG CACACCCGGG TGGACCTGCA
1051 ATTCTTGATC AAGTAGAACA AAAGCTAGCC TTGAAGCCCG AAAAGATGAG
1101 GGCCACGAGG GAAGTTCTAA GTGAATATGG AAACATGTCA AGCGCATGTG
1151 TATTGTTTCAT CTTAGATGAG ATGCGGAAGA AATCGGCTCA AAATGGACTT
1201 AAGACAAC TG GAGAAGGACT TGATTGGGGT GTGTTGTTTCG GCTTCGGACC
1251 AGGACTTACC ATTGAAACCG TTGTTCTTCG TAGCGTGGCT ATATAAGATG
1301 TGTGATTGTT TTTATTTTAA TGTATTACTT TTAATCTTGC TGCCTTGAAT
1351 TTCGATTTAA GAATAAATAA ATATATCTTT TGATAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CGAATTC

FIGURE 2

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1 MVSVAEIRKA QRAEGPATIL AIGTANPPNR VEQSTYPDFY FKITNSEHKT
51 ELKEKFQRM C DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSL V GQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNIN KALVEAFQPL GISDYN SIFW
301 IAHPGGPAIL DQVEQKLALK PEKMRATREV LSEYGNMSSA CVLFILDEMR
351 KKS AQNGLKT TGEGLDWGVL FGFGPGLTIE TVVLR SVAI

FIGURE 3

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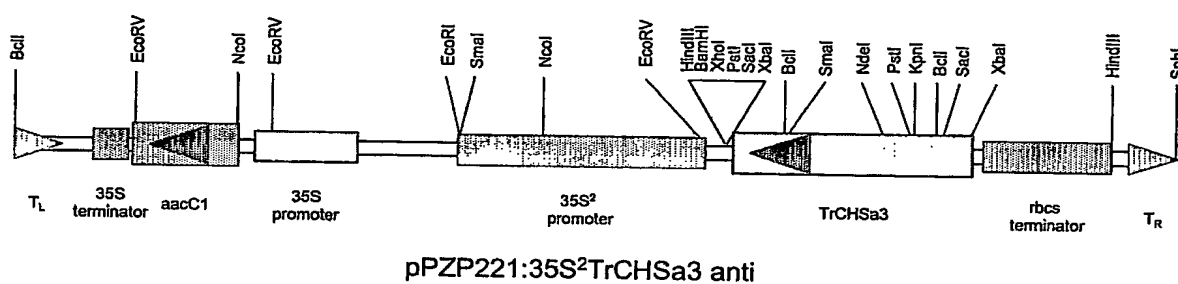
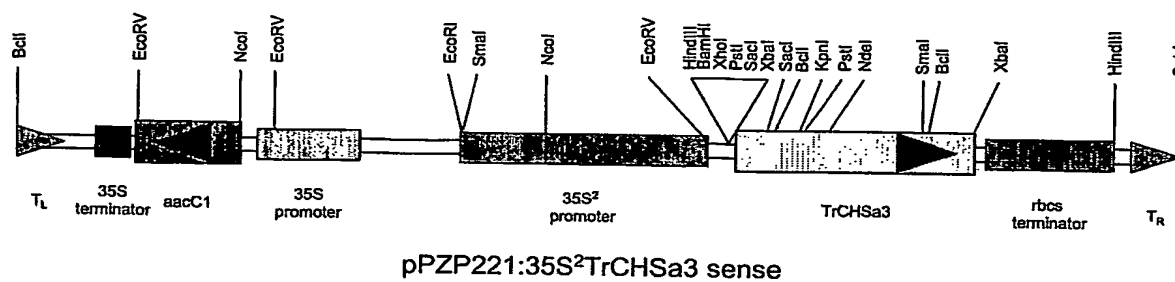
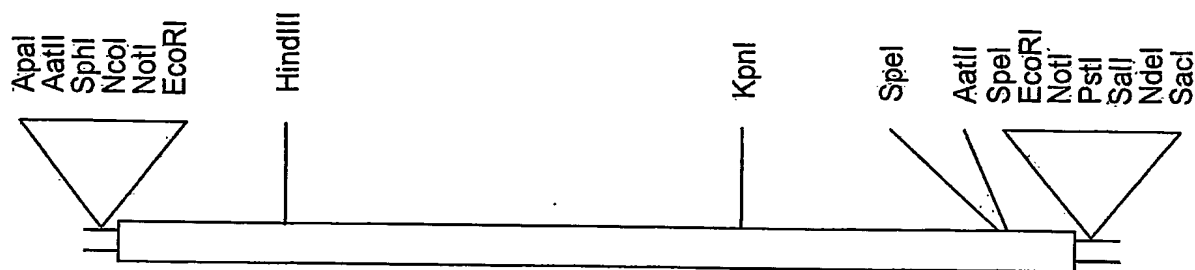


FIGURE 4

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TrCHSc

FIGURE 5

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1 GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GATTCAATCT
51 GTTGTGCATA AAATTCACCTC ATTGCATAGA AAACCATACA CATTTGATCT
101 TGCAAAGAAG AAATATGGGA GACGAAGGTA TAGTGAGAGG TGTCACAAAG
151 CAGACAACCC CTGGGAAGGC TACTATATTG GCTCTTGGCA AGGCATTCCC
201 TCACCAACTT GTGATGCAAG AGTGTTTAGT TGATGGTTAT TTTAGGGACA
251 CTAATTGTGA CAATCCTGAA CTTAAGCAGA AACTTGCTAG ACTTTGTAAG
301 ACAACCACGG TAAAAACAAG GTATGTTGTT ATGAATGAGG AGATACTAAA
351 GAAATATCCA GAACTTGTTG TCGAAGGCGC CTCAACTGTA AAACAACGTT
401 TAGAGATATG TAATGAGGCA GTAACACAAA TGGCAATTGA AGCTTCCCAA
451 GTTTGCCTAA AGAATTGGGG TAGATCCTTA TCGGACATAA CTCATGTGGT
501 TTATGTTTCA TCTAGTGAAG CTAGATTACC CGGTGGTGAC CTATACTTGT
551 CAAAAGGACT AGGACTAAAC CCTAAAATTC AAAGAACCAT GCTCTATTTT
601 TCTGGATGCT CGGGAGGCGT AGCCGGCCTT CGCGTTGCGA AAGACGTAGC
651 TGAGAACAAC CCTGGAAGTA GAGTTTTGCT TGCTACTTCG GAAACTACAA
701 TTATTGGATT CAAGCCACCA AGTGTTGATA GACCTTATGA TCTTGTTGGT
751 GTGGCACTCT TTGGAGATGG TGCTGGTGCA ATGATAATTG GCTCAGACCC
801 GGTATTTGAA ACTGAGACAC CATTGTTTGA GCTGCATACT TCAGCTCAGG
851 AGTTTATACC AGACACCGAG AAGAAAATTG ATGGGCGGCT GACGGAGGAG
901 GGCATAAGTT TCACACTAGC AAGGGAACCT CCGCAGATAA TCGAAGACAA
951 TGTTGAGGGA TTCTGTAATA AACTAATTGA TGTTGTTGGG TTGGAGAATA
1001 AGGAGTACAA TAAGTTGTTT TGGGCTGTGC ATCCAGGTGG GCCTGCGATA
1051 TTGAATCGCG TGGAGAAGCG GCTTGAGTTG TCGCCGCAGA AGCTGAATGC
1101 TAGTAGAAAA GCTCTAATGG ATTATGGAAA TGCTAGCAGC AATACTATTG
1151 TTTATGTGCT GGAATATATG CTAGAAGAGG AAAAGAAGAT TAAAAAGGCG
1201 GGTGGAGGAG ATTCTGAATG GGGATTGATA CTTGCTTTTG GACCTGGAAT
1251 TACTTTTGAG GGGATTCTAG CAAGGAACCT GTGTGCATGA AGTCTTATAC
1301 AATTGTGATG CATGACTTAT ACTCTTATTT CTACTAATTA TTATATTAAG
1351 CAAATTCAGA ACTTTTAAGT AATGATTTAA TGAAGAATAC TTATAGTATA
1401 TTGACTTTAT TCACTTTCAA AGCAAGTTTA TGATCCTAAG ACATGGTAGA
1451 ACTTGAGCAT GTGGAATAGT TGTAACAAAA ACTCTAAGCA AATAGAGACT
1501 TTATGTAGTA TAAAGCATTT CCAGACATGA TAAATAATGG TACCTCAGAA
1551 CATAAAATAT ATTTAGCTAT CTTTCATCCC CAACTTTACA CATCCACCAA
1601 GGTACAGAAT AAGCATATGT CAACACAAAA TGTAAGCTAA GTCTAACATG
1651 AGTAACCAAA CATGATGCCT GATTAAAGTTA AAAGAAAAGA AAATCTGAGG
1701 GCATAGATCT TCAATCACAC CACTCCAGAG GGAAGGCGTA GAACAAGCTG

FIGURE 6

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1751 TCCGCCGAAA ACACTGCAAT TCAATAAATA TCATTAGGAC AACAGTGCAG
1801 AGTCATGCGG GAAATGTCTT AAGTCACTGT ACTAAAAATA TAGGATTATA
1851 TTATGAACTA TACTAACCTT TTCACATAAT AGTAACAGAA ATCAGCTAAG
1901 ATGAATGTCT GGACAATTTC TGAGATAAGA ACCATGACGG CCATAAGCCA
1951 TACCCCAAGG CAACCAATAA ATGTCCACGG GTATCTAACA CCTGTTGCAA
2001 GAAATAGTAA GTTATTAGGA GATGTGCGGT TACGAAATTC AAGCTACACA
2051 ACAAAGGAG GCCAGAACAA CAGCAATCTT GTAACCAGAT GACAACAATA
2101 AAATGTAAAC TTAAAGAGAC CGAACACACA AACATTGCAA CTCAGATGGA
2151 ATTGCTGCCA TGTAAGTAGT AGGAGATTTG GGACGTCAAA TCAGTATATT
2201 ATGCAAATAC AAGGTATGAC CGCCTTGTCT ATTGTAGCAT ACAACAAACG
2251 TACAGTGGGT TTGTCCCTCT CAAAATGGCA GGATCTTTAC AGCACAATAT
2301 TTGGTTTTGT CATACTTATA CCATAAAAAA AAAAAAAAAA AAAAAAAAAA
2351 AAAGTACTCT GCGTTGTTAC CACTGCTTAA TCACTAGTGA ATTC

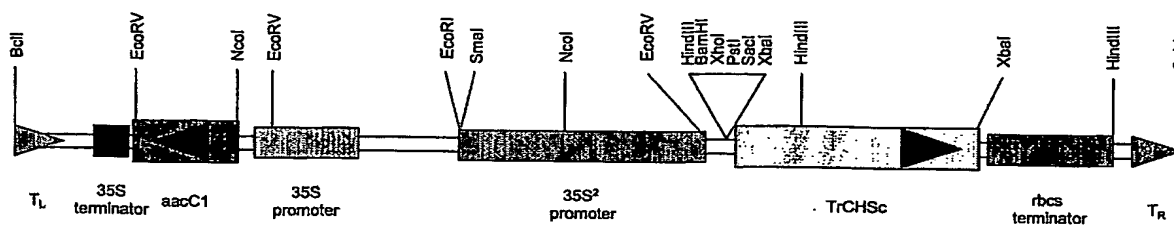
FIGURE 6 (cont.)

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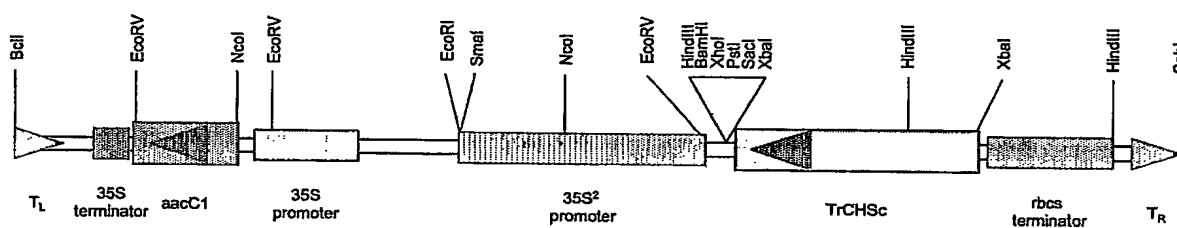
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51 PELKQKLARL CKTTTVKTRY VVMNEEILKK YPELVVEGAS TVKQRLEICN
101 EAVTQMAIEA SQVCLKNWGR SLSDITHVY VSSSEARLPG GDLYLSKGLG
151 LNPKIQR TML YFSGCSGGVA GLRVAKDVAE NNPGSRVLLA TSETTIIGFK
201 PPSVDRPYDL VGVALFGDGA GAMIIGSDPV FETETPLFEL HTSAQEFIPD
251 TEKKIDGRLT EEGISFTLAR ELPQIIEDNV EGFCNKLIDV VGLENKEYNK
301 LFWAVHPGGP AILNRVEKRL ELSPQKLNAS RKALMDYGNA SSNTIVYVLE
351 YMLEEEKKIK KAGGGDSEWG LILAFGPGIT FEGILARNLC A

FIGURE 7

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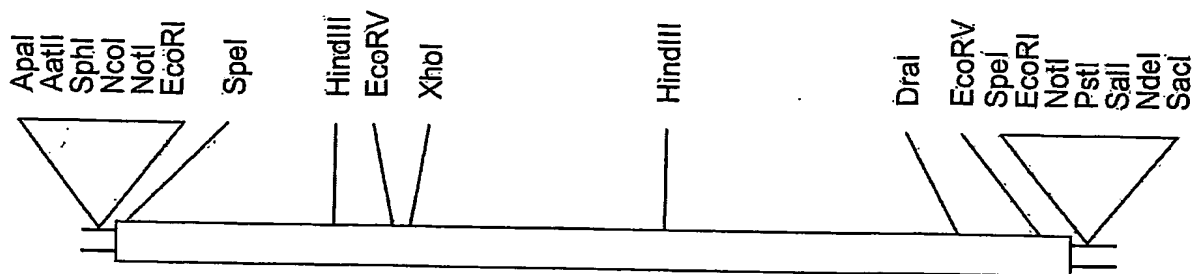
pPZP221:35S²TrCHSc sense



pPZP221:35S²TrCHSc anti

FIGURE 8

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TrCHSf

FIGURE 9

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1 GAATTCGATT AAGCAGTGGT AACACGCAG AGTACGCGGG ACTAAGCCTT
 51 GATTCATTGT TTGTTTCCAT AACACAAGAA CTAGTGTTTG CTTGAATCTT
 101 AAGAAAAAAT GCCTCAAGGT GATTTGAATG GAAGTTCCTC GGTGAATGGA
 151 GCACGTGCTA GACGTGCTCC TACTCAGGGA AAGGCAACGA TACTTGCAAT
 201 AGGAAAGGCT TTCCCCGCCC AGGTCCTCCC TCAAGAGTGC TTGGTGGAAG
 251 GATTCATTCTG CGACACTAAG TGTGACGATA CTTATATTAA GGAGAAATTG
 301 GAGCGTCTTT GCAAAAACAC AACTGTGAAA ACAAGATACA CAGTAATGTC
 351 AAAGGAGATC TTAGACAACCT ATCCAGAGCT AGCCATAGAT GGAACACCAA
 401 CAATAAGGCA AAAGCTTGAA ATAGCAAATC CAGCAGTAGT TGAAATGGCA
 451 ACAAGAGCAA GCAAAGATTG CATCAAAGAA TGGGGAAGGT CACCTCAAGA
 501 TATCACACAC ATAGTCTATG TTTCTCGAG CGAAATTTCG CTACCCGGTG
 551 GTGACCTTTA TCTTGCAAAT GAACTCGGCT TAAACAGCGA TGTTAATCGC
 601 GTAATGCTCT ATTTCTCGG TTGCTACGGC GGTGTCCTG GCTTACGTGT
 651 CGCCAAAGAC ATCGCCGAAA ATAACCCTGG TAGTAGGGTG TTACTCACAA
 701 CATCCGAGAC CACTATTCTC GGTTTTTCGAC CACCGAGTAA AGCTAGACCT
 751 TATGACCTCG TTGGCGCTGC ACTTTTCGGT GATGGCGCCG CTGCTGCAAT
 801 AATTGGAACA GACCCTATAT TGAATCAAGA ATCACCTTTC ATGGAATTGA
 851 ACCATGCAGT CCAAAAATTC TTGCCTGATA CACAAAATGT GATTGATGGT
 901 AGAATCACTG AAGAGGGTAT TAATTTTAAG CTTGGAAGAG ACCTTCCTCA
 951 AAAAATTGAA GACAATATTG AAGAATTTTG CAAGAAAATT ATGGCTAAAA
 1001 GTGATGTTAA GGAATTTAAT GACTTATTTT GGGCTGTTCA TCCTGGTGGG
 1051 CCAGCTATAC TCAATAAGCT AGAAAATATA CTCAAATTGA AAAGTGATAA
 1101 ATTGGATTGT AGTAGGAAGG CATTAATGGA TTATGGAAAT GTTAGTAGCA
 1151 ATACTATATT CTATGTGATG GAGTATATGA GAGATTATTT GAAGGAAGAT
 1201 GGAAGTGAAG AATGGGGATT AGGATTGGCT TTTGGACCAG GGATTACTTT
 1251 TGAAGGGGTT CTCCTCCGTA GCCTTTAATC TTGAAATAAT AATTCATATG
 1301 AAATTACTTG TCTTAAGATT GTGATAGGAA GATGAATATG TATTGGATTA
 1351 ATATTGATAT GGTGTTATTT TAAGTTGATT TTAAAAAAG TTTATTAAATA
 1401 AAGTATGATG TAACAATTGT TGTTTGAATG TTAAAAGGGA AGTATACTAT
 1451 TTTAAGTTCT TGACCATACT GATTTTTTCT TTACACATTT TCATATCTAA
 1501 AATTGTTCTA TGATATCTTC ATTGTTGATA CTGTAATAAT ATAATATCTA
 1551 ATTTGGCTGG CAAAATGAAA GATTTTTTCAC CGAAAAAAA AAAAAAAA
 1601 AAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CACTAGTGAA
 1651 TTC

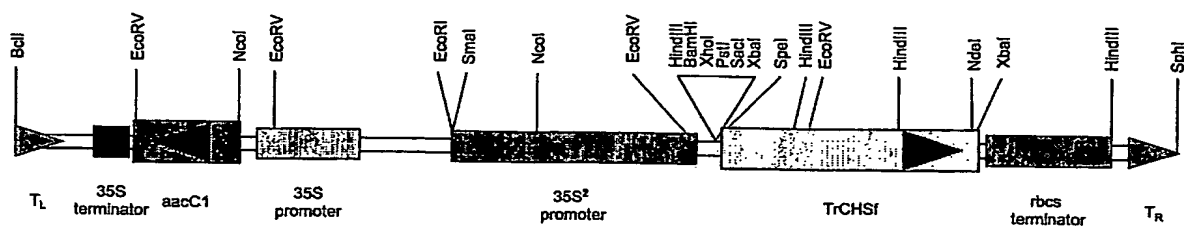
FIGURE 10

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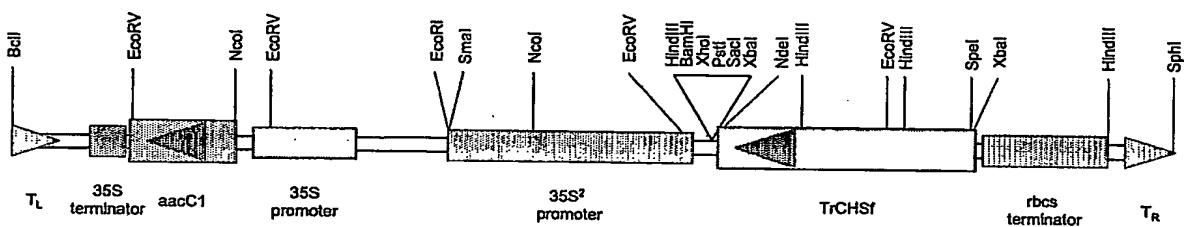
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51 RDTKCDDTYI KEKLERLCKN TTVKTRYTVM SKEILDNYPE LAIDGTPTIR
101 QKLEIANPAV VEMATRAS KD CIKEWGRSPQ DITHIVYVSS SEIRLPGGDL
151 YLANELGLNS DVNRVMLYFL GCYGGVTGLR VAKDIAENNP GSRVLLTTSE
201 TTILGFRPPS KARP YDLVGA ALFGDGAAAA IIGTDPILNQ ESPFMELNHA
251 VQKFLPDTQN VIDGRITEEG INFKLGRDLP QKIEDNIEEF CKKIMAKSDV
301 KEFN DLFWAV HPGGPAILNK LENILKLKSD KLDCSRKALM DYGNVSSNTI
351 FYVMEYMRDY LKEDGSEEWG LGLAFGPGIT FEGVLLRSL

FIGURE 11

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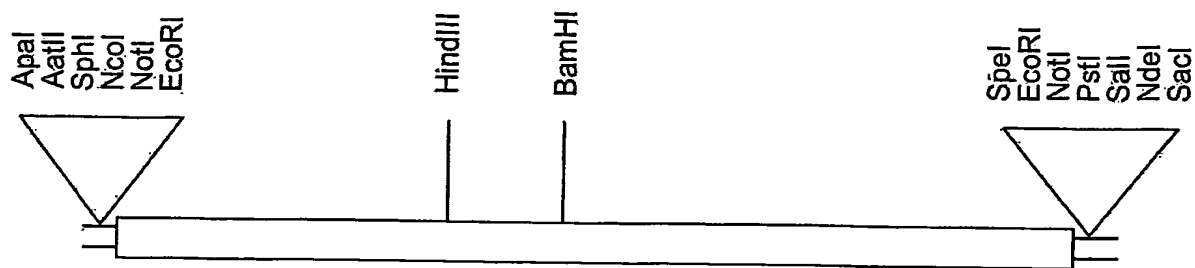
pPZP221:35S²TrCHSf sense



pPZP221:35S²TrCHSf anti

FIGURE 12

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TrCHSh

FIGURE 13

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1 GAATTCAC TA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGGAA
51 TCCACCAAAT CAACACCATT AATAACCTTC CAAATTCTCG TTACCTCACC
101 AAATCTCATT TTTCATTATA TATCTTGGGT ACATCTTTTG TTACCTCCAA
151 CAAAAAATG GTGACCGTAG AAGAGATTCG TAACGCCCAA CGTTCAAATG
201 GCCCTGCCAC TATCTTAGCT TTTGGCACAG CCACTCCTTC TAACGTGTGC
251 ACTCAAGCTG ATTATCCTGA TTACTACTTT CGTATCACCA ACAGCGAACA
301 TATGACTGAT CTTAAGGAAA AATTCAAGCG GATGTGTGAT AGATCAATGA
351 TAAAGAAACG TTACATGCAC CTAACAGAAG ACTTTCTGAA GGAGAATCCA
401 AATATGTGTG AATACATGGC ACCATCACTA GATGTAAGAC GAGACATAGT
451 GGTGTGTGAA GTACCAAAGC TAGGTAAAGA AGCAGCAAAA AAAGCCATAT
501 GTGAATGGGG ACAACCAAAA TCCAAAATCA CACATCTTGT TTTCTGCACC
551 ACTTCCGGTG TTGACATGCC GGGAGCCGAT TACCAACTCA CCAAACTTTT
601 AGGCTTAAAA CTTTCTGTCA AGCGTCTCAT GATGTATCAA CAAGGTTGTT
651 TCGCTGGCGG CACAGTTCTC CGCTTAGCAA AAGACCTTGT TGAGAATAAC
701 AAAAATGCAA GAGTTCTTGT TGTTTGTCTT GAAATTACTG CGGTTACTTT
751 TCGTGGAACA TCGGATACTC ATCTTGATTC GCTCGTGGGA CAGGCGCTTT
801 TTGGTGATGG AGCCGCAGCA ATGATTATTG GTGCGGATCC TGATTTAACC
851 GTGGAGCGTC CGATTTTCGA GATTGTTTCG GCTGCTCAGA CTATTCTTCC
901 TGATTCTGAT GGCGCAATTG ATGGACATCT TCGTGAAGTG GGGCTCACTT
951 TTCATTTATT GAAAGATGTT CCGGGGATTA TTTCAAAGAA CATTGAAAAA
1001 AGTTTAGTTG AAGCTTTTGC GCCTATTGGG ATTAATGATT GGAACCTAAT
1051 ATTTTGGGTT GCACATCCAG GTGGACCGGC TATTTTAGAC CAGGTTGAAG
1101 AGAAACTCCA TCTTAAAGAG GAGAAACTCC GGTCCACCCG GCATGTGCTT
1151 AGTGAATATG GAAATATGTC AAGTGCATGT GTTTTATTTA TTTTGGATGA
1201 AATGAGAAAG AGGTCTAAAG AGGAAGGGAT GATTACAACCT GGTGAAGGGT
1251 TGGAATGGGG TGTGTTGTTT GGGTTTGGAC CGGGTTTAAC TGTTGAAACC
1301 GTTGTGCTTC ATAGTGTTCC GGTTCAAGGT TGAATTTATT ATACATAGAT
1351 TGGAATAATA AATTGCTCTG CCGAGAGATG TGAACCTAAT TTGTAGGCAA
1401 GCTCAAATTA AAGTTTGAGA TAATATTGTG CTTTAGTTAT TATGGTATGT
1451 AATGTAATGT TTTTACTTTT TTCGAAATTC ATGTAATTTG ATATGTAAAG
1501 TAATATGTTT GGGTTGGAAT ATAATTATTT GTTAACTAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAGTACT CTGCGTTGTT ACCACTGCTT AATCGAATTC

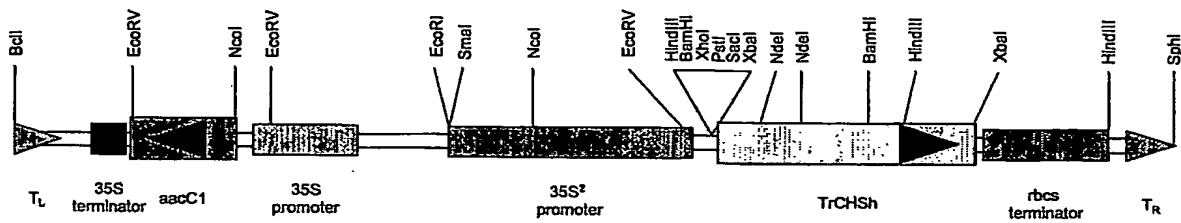
FIGURE 14

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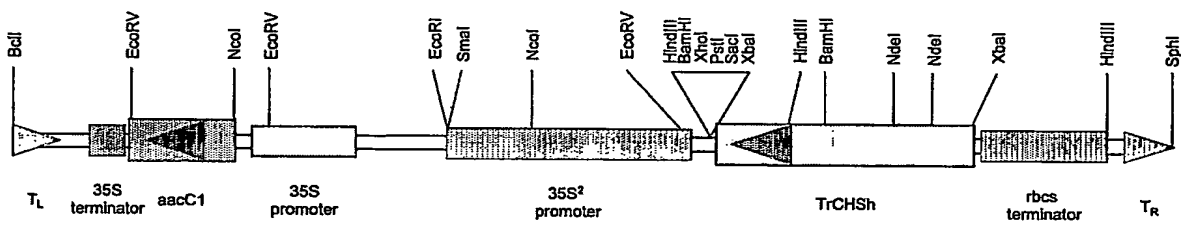
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51 DLKEKFKRMC DRSMIKKRYM HLTEDFLKEN PNMCEYMAPS LDVRRDIVVV
101 EVPKLGKEAA KKAICEWGQP KSKITHLVFC TTSGVDMPGA DYQLTKLLGL
151 KPSVKRLMMY QQGCFAGGTV LRLAKDLVEN NKNARVLVVC SEITAVTFRG
201 PSDTHLDSLV GQALFGDGAA AMIIGADPDL TVERPIFEIV SAAQTILPDS
251 DGAIDGHLRE VGLTFHLLKD VPGIISKNIE KSLVEAFAPI GINDWNSIFW
301 VAHPGGPAIL DQVEEKLHLK EEKLRSTRHV LSEYGNMSSA CVLFILDEMR
351 KRSKEEGMIT TGEGLEWGV LFGFGPGLTVE TVVLHSVPVQ G

FIGURE 15

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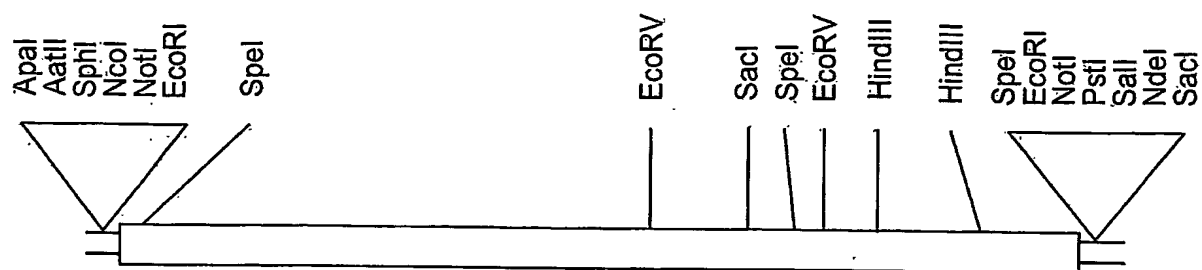
pPZP221:35S²TrCHSh sense



pPZP221:35S²TrCHSh anti

FIGURE 16

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TrBANa

FIGURE 17

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1 GAATTCGATT AAGCAGTGGT AACACGCAG AGTACGCGGG ATAAAACTG
51 CACTAGTGTG TATAAGTTTC TTGGTGAAAA AAGAGTTTGT AAATTAACAT
101 CATGGCTAGT ATCAAACAAA TTGGAAACAA GAAAGCATGT GTGATTGGTG
151 GCACTGGTTT TGTTGCATCT ATGTTGATCA AGCAGTTACT TGAAAAGGGT
201 TATGCTGTTA ATACTACCGT TAGAGACCCA GATAGCCCTA AGAAAATATC
251 TCACCTAGTG GCACTGCAAA GTTTGGGGGA ACTGAATCTA TTTAGAGCAG
301 ACTTAACAGT TGAAGAAGAT TTTGATGCTC CTATAGCAGG ATGTGAACTT
351 GTTTTTCAAC TTGCTACACC TGTGAACTTT GCTTCTCAAG ATCCTGAGAA
401 TGACATGATA AAGCCAGCAA TCAAAGGTGT GTTGAATGTG TTGAAAGCAA
451 TTGCAAGAGC AAAAGAAGTT AAAAGAGTTA TCTTAACATC TTCGGCAGCC
501 GCGGTGACTA TAAATGAACT CAAAGGGACA GGTCAATGTTA TGGATGAAAC
551 CAACTGGTCT GATGTTGAAT TTCTCAACAC TGCAAAACCA CCCACTTGGG
601 GTTATCCTGC CTCAAAAATG CTAGCTGAAA AGGCTGCATG GAAATTTGCT
651 GAAGAAAATG ACATTGATCT AATCACTGTG ATACCTAGTT TAACAACTGG
701 TCCTTCTCTC ACACCAGATA TCCCATCTAG TGTGGGCTTG GCAATGTCTC
751 TAATAACAGG CAATGATTTT CTCATAAATG CTTTGAAAGG AATGCAGTTT
801 CTGTCGGGTT CGTTATCCAT CACTCATGTT GAGGATATTT GCCGAGCTCA
851 TATATTTCTT GCAGAGAAAG AATCAGCTTC TGGTAGATAC ATTTGCTGTG
901 CTCACAATAC TAGTGTTCCC GAGCTTGCAA AGTTTCTCAA CAAACGATAT
951 CCTCAGTATA AAGTTCCAAC TGAATTTGAT GATTGCCCCA GCAAGGCAAA
1001 GTTGATAATC TCTTCTGAAA AGCTTATCAA AGAAGGGTTC AGTTTCAAGC
1051 ATGGTATTGC CGAAACTTTC GACCAGACTG TCGAGTATTT TAAGACTAAG
1101 GGGGCACTGA AGAATTAGAT TTTGATATTT CTAATTC AATGAATAAG
1151 AAGCTTGTTA TGTGTTTGTG AAGTTCAGAG TGAAATATCA AATGAATAAG
1201 TGGAGAGAGC ACAATAAGAG GAGAGCACAA TAATTTTGGG AAAAAAAAAA
1251 AAAAAAAAAA AAAAAAAGT ACTCTGCGTT GTTACCCTG CTTAATCACT
1301 AGTGAATTC

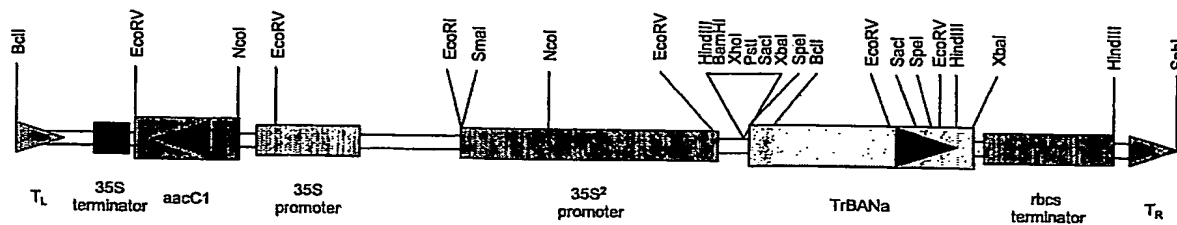
FIGURE 18

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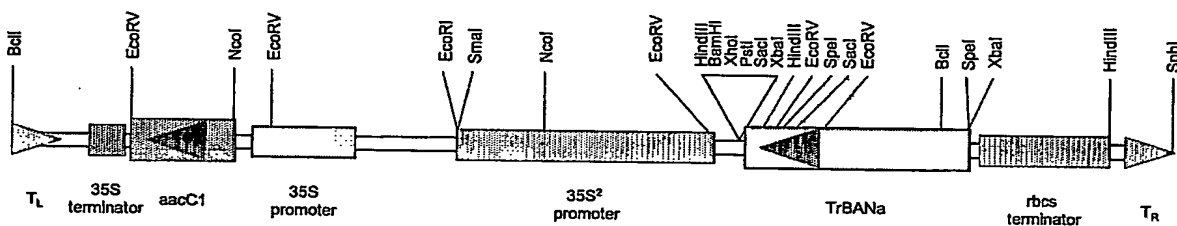
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101 DMIKPAIKGV LNVLKAIARA KEVKRVILTS SAAAVTINEL KGTGHVMDDET
151 NWSDV EFLNT AKPPTWGYP A SKMLAEKAAW KFAEENDIDL ITVIPS LTG
201 PSLTPDIPSS VGLAMSLITG NDFLINALKG MQFLSGSLSI THVEDICRAH
251 IFLAEKESAS GRYICCAHNT SVPELAKFLN KRYPQYKVPT EFDDCPSKAK
301 LIISSEKLIK EGFSFKHGIA ETFDQTV EYF KTKGALKN

FIGURE 19

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pPZP221:35S²TrBANa sense



pPZP221:35S²TrBANa anti

FIGURE 20

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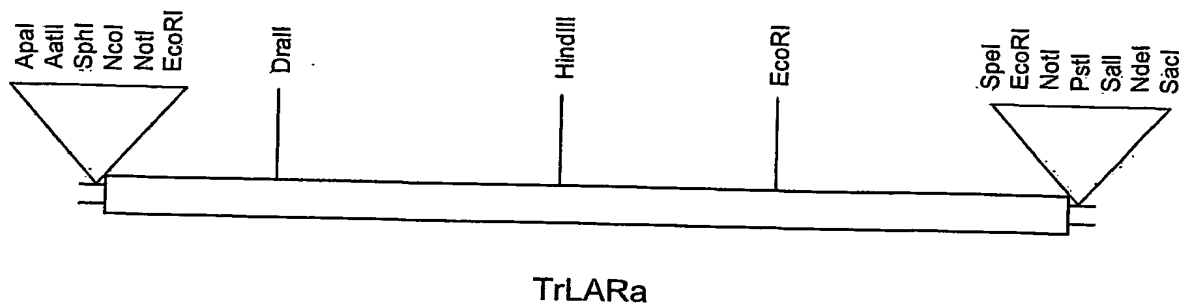


FIGURE 21

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1 GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GATACCAACA
51 TTGTCACAAT TAACTCTAAA AGCAAAGCAA TGGCACCAGC AGCAACATCA
101 TCACCAACCA CTCCTACTAC TACCAAGGGT CGTGTCTTAA TTGTTGGAGG
151 AACAGGTTTC ATTGGAAAAT TTGTAACCTGA GGCAAGTCTT TCCACAACAC
201 ACCCAACCTA CTTGTTGGTT CGGCCAGGAC CTCTTCTCTC TTCTAAGGCT
251 GCCACTATTA AGGCATTCCA AGAGAAAGGT GCCATTGTCA TTTATGGTCG
301 GGTAAATAAT AAGGAGTTCA TGGAGATGAT TTTGAAAAAG TATGAGATAA
351 ATGTAGTCAT TTCTGCAATA GGAGGCTCTG ATGGCTTGCT GGAACAGCTT
401 ACTTTGGTGG AGGCCATGAA ATCTATTAAC ACCATTAAGA GGTTTTTGCC
451 TTCGGAATTT GGTCACGATG TGGACAGAGC AAATCCTGTG GAACCTGGCC
501 TAACAATGTA CAAACAGAAA CGTTTGGTTA GACGTGTGAT CGAAGAATCT
551 GGTATACCAT ACACCTACAT CTGTTGCAAT TCGATCGCAT CTTGGCCGTA
601 CTATGACAAT TGTCATCCAT CACAGCTTCC TCCACCGTTG GATCAATTAC
651 ATATTTATGG TCATGGCGAT GTCAAAGCTT ACTTTGTTGA TGGCTATGAT
701 ATTGGGAAAT TCACAATGAA GGTCATTGAT GATGAAAGAA CAATCAACAA
751 AAATGTTTAT TTTTCGACCTT CTAACAATTG TTATAGCATG AATGAGCTTG
801 CTTCTTTGTG GGAAAACAAA ATTGCACGAA AAATTCCTAG AGTGATCGTC
851 TCTGAAGACG ATCTTCTAGC AATAGCCGCA GAAAATTGCA TACCGGAAAG
901 TGTCGTGGCA CCAATCACTC ATGATATATT CATCAATGGA TGTCAAGTTA
951 ACTTCAAGAT AGATGGAATT CATGATGTTG AAATTGGCAC TCTATATCCT
1001 GGTGAATCGG TAAGAAGTTT GGAGGAATGC TATGAGAAAT TTGTTGTCAT
1051 GGCGGCTGAC AAGATTCATA AAGAAGAAAC TGGAGTTACC GCAGGTGGGG
1101 GCGGCACAAC GGCTATGGTA GAGCCGGTGC CAATCACAGC TTCCTGTTGA
1151 AAAGGTTTAC CTGAGGTGGA TATTCTTTTG AGTCATAAGA CATGTTGATT
1201 GTTGATGTTG TTTTCAAGAA TGTTTCATCA TTTCATGTGT TTTATTAATC
1251 CTAAGTACAA ATAATTGCTG TCTACGTACG TTCTTAGTTG CAAAAATTCT
1301 TGTTATTCTC TATTGAGGTA AAAGTCTTCA TGTTTACAAA AAAAAAAAAA
1351 AAAAAAAAAA AAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1401 AGTGAATTC

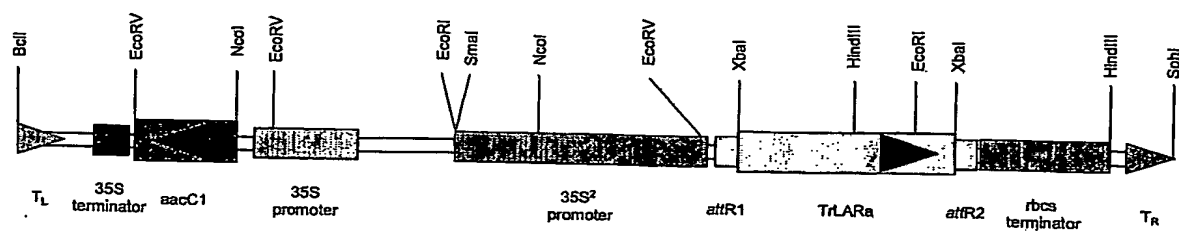
FIGURE 22

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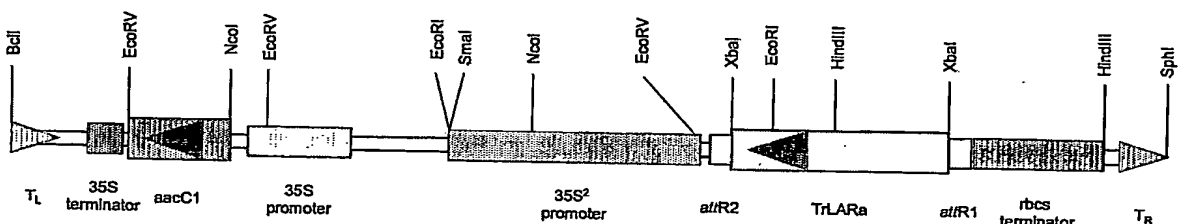
1 MAPAATSSPT TPTTTKGRVL IVGGTGFIGK FVTEASLSTT HPTYLLVRPG
51 PLLSSKAATI KAFQEKGAIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRANPVEPG LTMYKQKRLV
151 RRVIEESGIP YTYICCNLSIA SWPYVDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIAR
251 KIPRVIVSED DLLAIAAENC IPESVVAPIT HDIFINGCQV NFKIDGIHDV
301 EIGTLYPGES VRSLEECYEK FVMAADKIH KEETGVTAGG GGTAMVEPV
351 PITASC

FIGURE 23

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pPZP221:35S²TrLARa sense



pPZP221:35S²TrLARa anti

FIGURE 24

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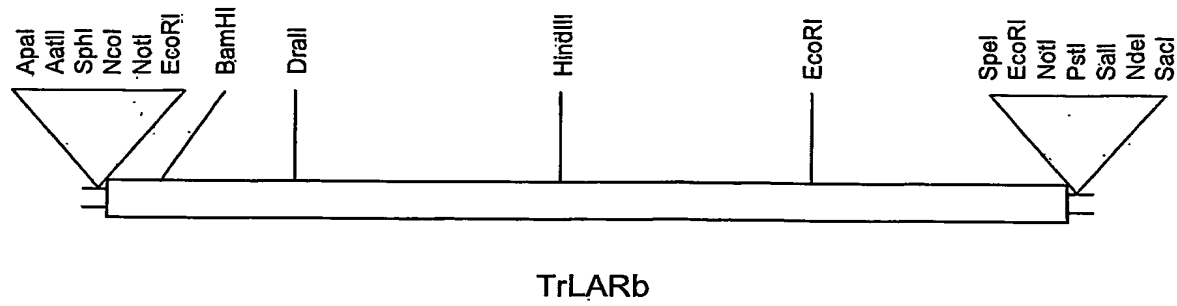


FIGURE 25

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1 GAATTCGATT AAGCAGTGGT AACACGCAG AGTACGCGGG AGGATCCTTC
 51 CATTTTGCAT ACCAACATTG TCACAATTAA CTCTAAAAGC AAAGCAATGG
 101 CACCAGCAGC AACATCATCA CCAACCACTC CTACTACTAC CAAGGGTCGT
 151 GTCCTAATTG TTGGAGGAAC AGGTTTCATT GGAAAATTTG TAACTGAGGC
 201 AAGTCTTTCC ACAACACACC CAACCTACTT GTTGGTTCGG CCAGGACCTC
 251 TTCTCTCTTC TAAGGCTGCC ACTATTAAGG CATTCCAAGA GAAAGGTGCC
 301 ATTGTCATTT ATGGTCGGGT AAATAATAAG GAGTTCATGG AGATGATTTT
 351 GAAAAAGTAT GAGATAAATG TAGTCATTTT TGCAATAGGA GGCTCTGATG
 401 GCTTGCTGGA ACAGCTTACT TTGGTGGAGG CCATGAAATC TATTAACACC
 451 ATTAAGAGGT TTTTGCCTTC AGAATTTGGT CACGATGTGG ACAGAGCAAA
 501 TCCTGTGGAA CCTGGCCTAA CAATGTACAA ACAGAAACGT TTGGTTAGAC
 551 GTGTGATCGA AGAATCTGGT GTACCATACA CCTACATCTG TTGCAATTGG
 601 ATCGCATCCT GGCCGTACTA TGACAATTGT CATCCATCAC AGCTTCCTCC
 651 ACCGTTGGAT CAATTACATA TTTATGGTCA TGGCGATGTC AAAGCTTACT
 701 TTGTTGATGG CTATGATATT GGGAAATTCA CAATGAAGGT CATTGATGAT
 751 GAAAGAACAA TCAACAAAAA TGTTCAATTT CGACCTTCTA ACAATTGTTA
 801 TAGCATGAAT GAGCTTGCTT CTTTGTGGGA AAACAAAATT GCACGAAAAA
 851 TTCCTAGAGT GATCGTCTCT GAAGACGATC TTCTAGCAAT AGCCGCAGAA
 901 AACTGCATAC CGGAAAGTGT TGTGGCATCA ATCACTCATG ATATATTCAT
 951 CAATGGATGT CAAGTAACT TCAAGGTAGA TGGAATTCAT GATGTTGAAA
 1001 TTGGCACTCT ATATCCTGGT GAATCGGTAA GAAGTTTGGA GGAATGCTAT
 1051 GAGAAATTTG TTGTCATGGC GGCTGACAAG ATTCATAAAG AAGAACTGG
 1101 AGTTACCGCA GGTGGGGGCG GCACAACGGC TATGGTAGAG CCGGTGCCAA
 1151 TCACAGCTTC CTGTTGAAAA GGTTACCTG AGGTGGATAT TCTTTTGAGT
 1201 CATAAGACAT GTTGATTGTT GATGTTGTTT TCAAGAATGT TTCATCATTT
 1251 CATGTGTTTT ATTAATCCTA AGTACAAATA ATTGCTGTCT ACGTACGTTT
 1301 TTAGTTGCGA AAATTCTTGT TATTCTCTAT TGGGGTAAAA GTCTTCATGT
 1351 TTATTGTAGT TGTGTTGGTT TTTCATATAT GCTATTTGCA ATAATGATTT
 1401 TTGTGAAGCA CTTGTGGTGT ATTTACTTAC TACTGAAAT AATGGTTACA
 1451 CAAAATATAT AAAAAAATAA AAATAAGCAA AAAAAAAAAA AAAAAAAAAA
 1501 AAAAAAAAAA GTA CTCTGCG TTGTTACCAC TGCTTAATCA CTAGTGAATT
 1551 C

FIGURE 26

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1 MAPAATSSPT TPTTTKGRVL IVGGTGFIGK FVTEASLSTT HPTYLLVRPG
51 PLLSSKAATI KAFQEKGAIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRANPVEPG LTMYKQKRLV
151 RRVIEESGVP YTYICCNLSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIAR
251 KIPRVIVSED DLLAIAAENC IPESVVASIT HDIFINGCQV NFKVDGIHDV
301 EIGTLYPGES VRSLEECYEK FVVMADKIH KEETGVTAGG GGTTAMVEPV
351 PITASC

FIGURE 27

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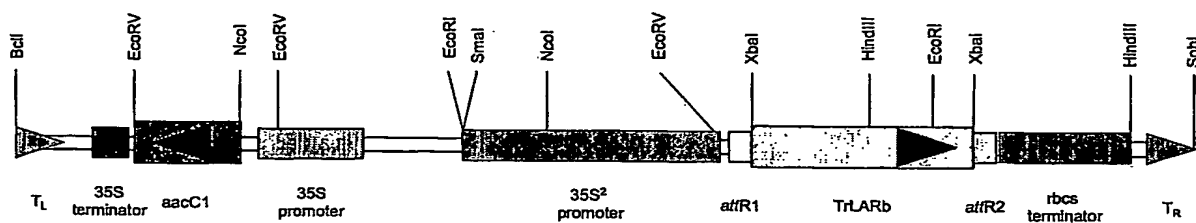
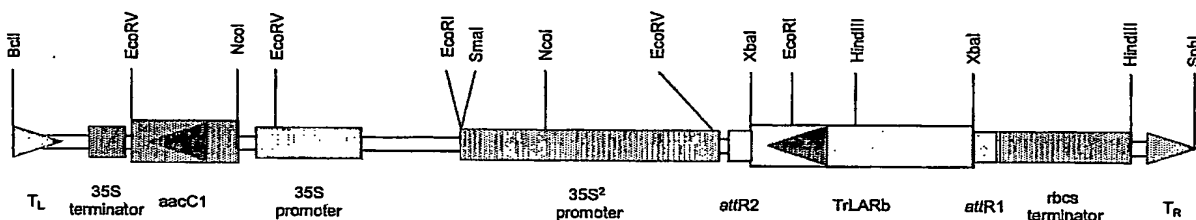
pPZP221:35S²TrLARb sensepPZP221:35S²TrLARb anti

FIGURE 28

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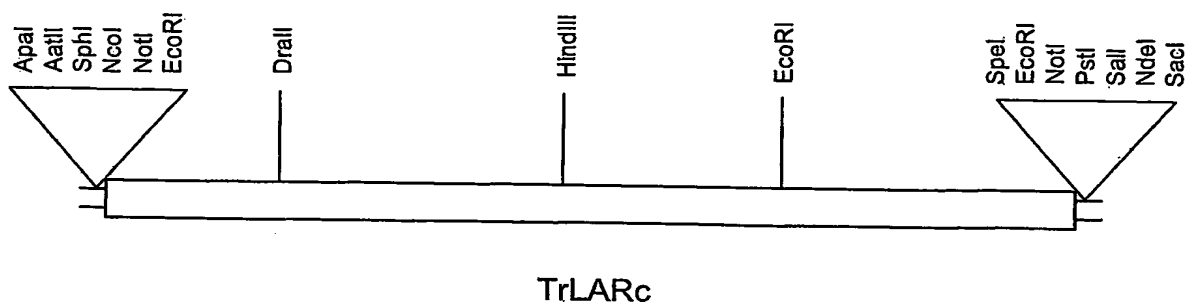


FIGURE 29

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1 GAATTCGATT AAGCAGTGGT AACCAACGCAG AGTACGCGGG GATACCAACA
51 TTGTCACAAT TAACTCTAAA AGTAAAGCAA TGGCACCAGC AGCAACATCA
101 TCACCAACCA CTCCCCTAC TACCAAGGGT CGTGTCTTAA TTGTTGGAGG
151 AACAGGTTTC ATTGGAAAAT TTGTAAGTGA GGCAAGTCTT TCCACAACAC
201 ACCCAACCTA CTTGTTGGTT CGGCCAGGAC CTCTTCTCTC TTCTAAGGCT
251 GCCACTATTA AGGCATTCCA AGAGAAAGGT GCCATTGTCA TTTATGGTCG
301 GGTAATAAAT AAGGAGTTCA TGGAGATGAT TTTGAAAAAG TATGAGATAA
351 ATGTAGTCAT TTCTGCAATA GGAGGCTCTG ATGGCTTGCT GGAACAGCTT
401 ACTTTGGTGG AGGCCATGAA ATCTATTAAC ACCATTAAGA GGTTTTTGCC
451 TTCGGAATTT GGTCACGATG TGGACAGAGC AGATCCTGTG GAACCTGGCC
501 TAACAATGTA CAAACAGAAA CGTTTGGTTA GACGTGTGAT CGAAGAATCT
551 GGTATACCAT ACACCTACAT CTGTTGCAAT TCGATCGCAT CTTGGCCGTA
601 CTATGACAAT TGTCATCCAT CACAGCTTCC TCCACCGTTG GATCAATTAC
651 ATATTTATGG TCATGGCGAT GTCAAAGCTT ACTTTGTTGA TGGCTATGAT
701 ATTGGGAAAT TCACAATGAA GGTCATTGAT GATGAAAGAA CAATCAACAA
751 AAATGTTTAT TTTTCGACCTT CTAACAATTG TTATAGCATG AATGAGCTTG
801 CTTCTTTGTG GGAAAACAAA ATTGCACGAA AAATTCCTAG AGTGATCGTC
851 TCTGAAGACG ATCTTCTAGC AATAGCCGCA GAAAATTGCA TACCGGAAAG
901 TGTCGTGGCA CCAATCACTC ATGATATATT CATCAATGGA TGTCAAGTTA
951 ACTTCAAGAT AGATGGAATT CATGATGTTG AAATTGGCAC TCTATATCCT
1001 GGTGAATCGG TAAGAAGTTT GGAGGAATGC TATGAGAAAT TTGTTGTCAT
1051 GGCGGCTGAC AAGATTCATA AAGAAGAAAC TGGAGTTACC GCAGGTGGGG
1101 GCGGCACAAC GGCTATGGTA GAGCCGGTGC CAATCACAGC TTCCTGTTGA
1151 AAAGGTTTAC CTGAGGTGGA TATTCTTTTG AGTCATAAGA CATGTTGATT
1201 GTTGATGTTG TTTTCAAGAA TGTTTCATCA TTTCATGTGT TTTATTAATC
1251 CTAAGTACAA ATAATTGCTG TCTACGTACG TTCTTAGTTG CAAAAATTCT
1301 TGTTATTCTC TATCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAGTACTCT
1351 GCGTTGTTAC CACTGCTTAA TCACTAGTGA ATTC

FIGURE 30

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1 MAPAATSSPT TPTTTKGRVL IVGGTGFIGN FVTEASLSTT HPTYLLVRPG
51 PLLSSKAATI KAFQEKGAIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRADPVEPG LTMYKQKRLV
151 RRVIEESGIP YTYICCNSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIAR
251 KIPRVIVSED DLLAIAAENC IPESVVAPIT HDIFINGCQV NFKIDGIHDV
301 EIGTLYPGES VRSLEECYEK FVMAADKIH KEETGVTAGG GGTAMVEPV
351 PITASC

FIGURE 31

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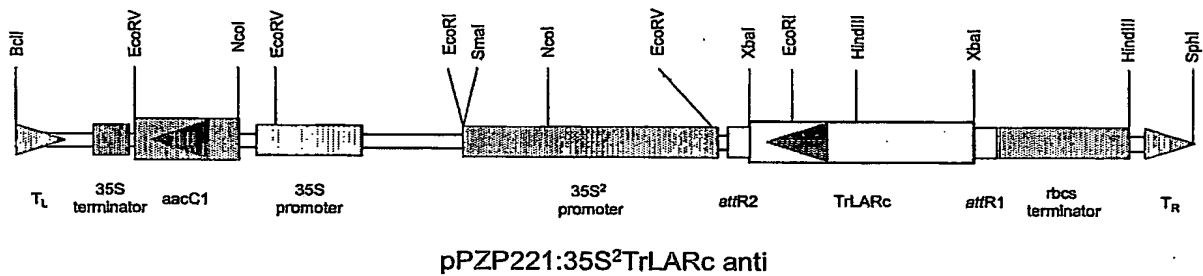
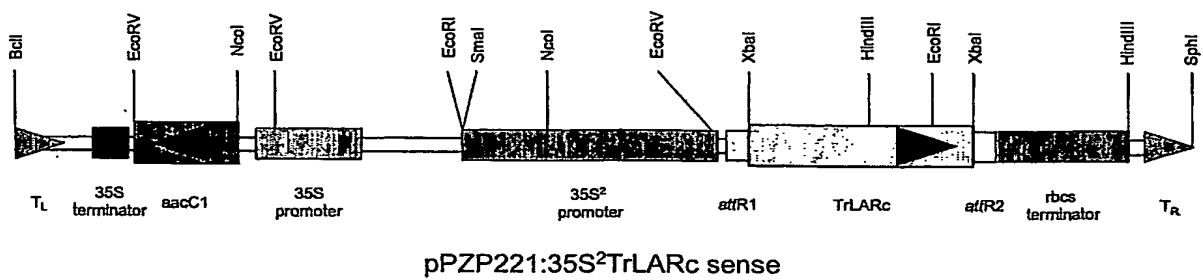


FIGURE 32

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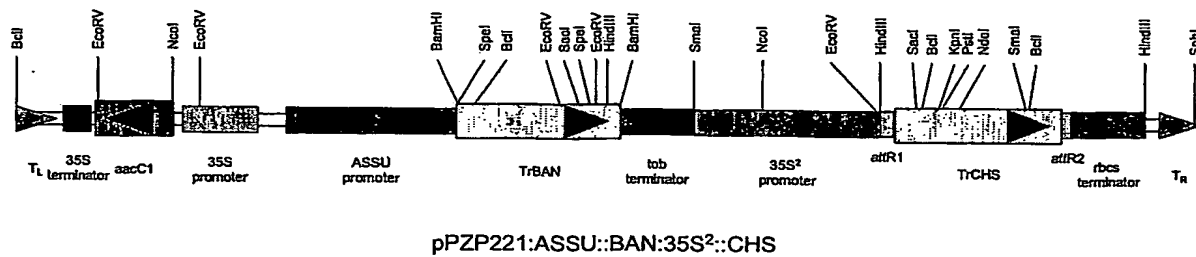


FIGURE 33

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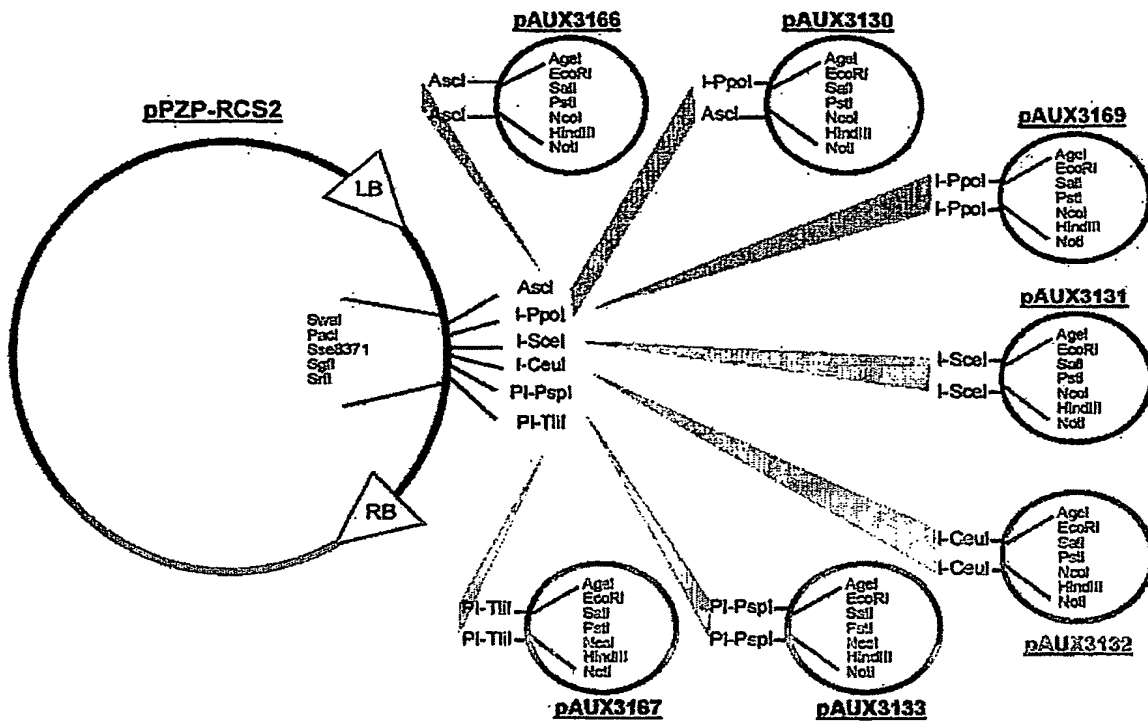


FIGURE 34

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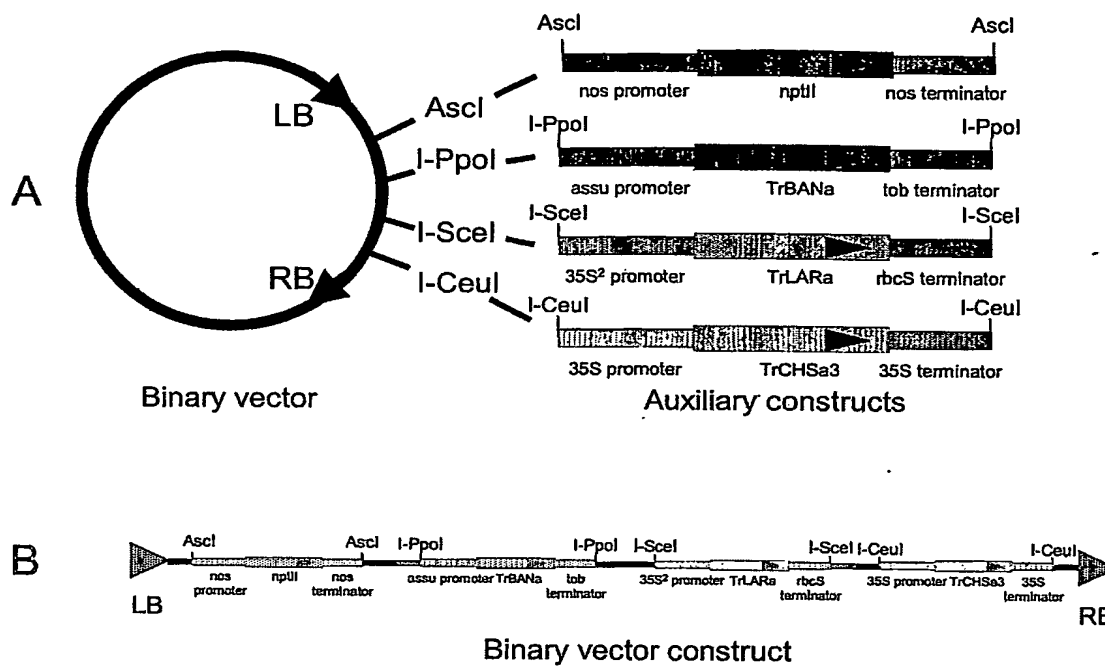


FIGURE 35

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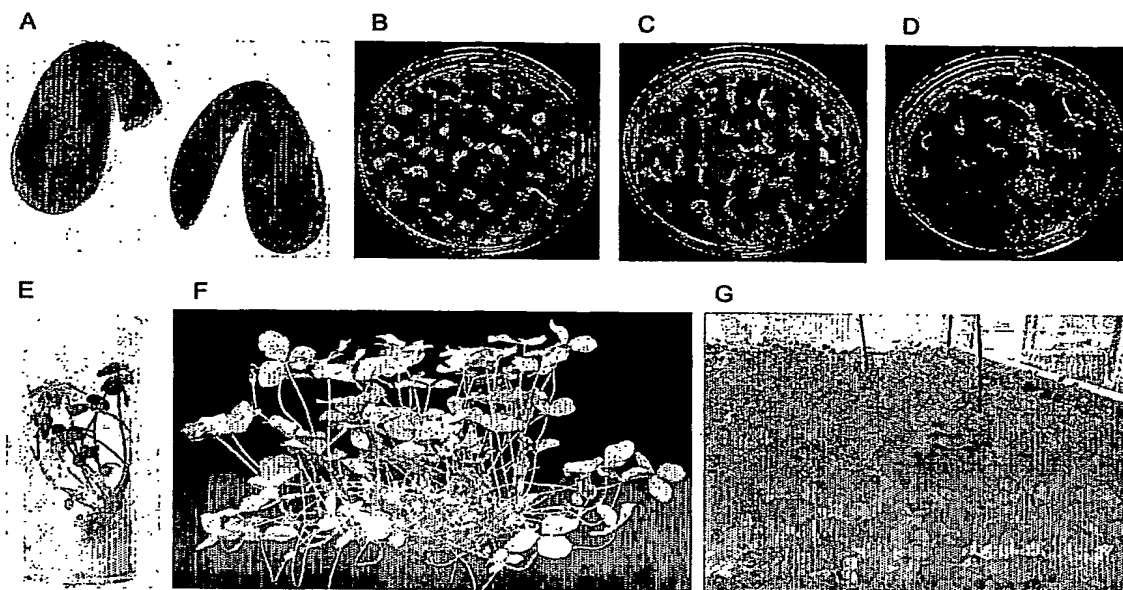


FIGURE 36

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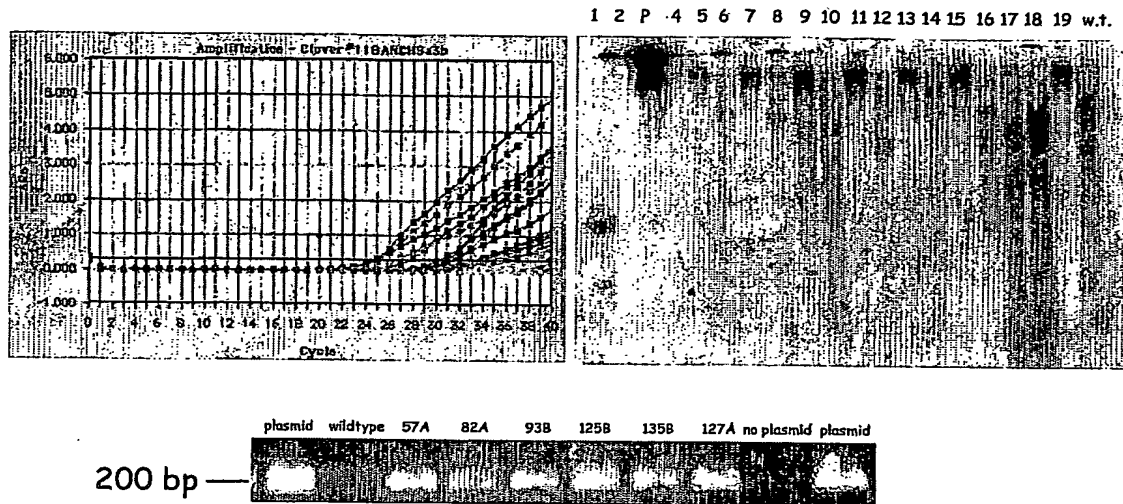
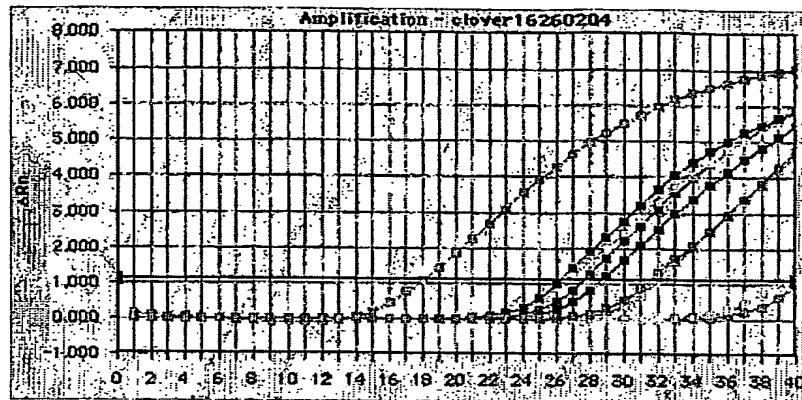
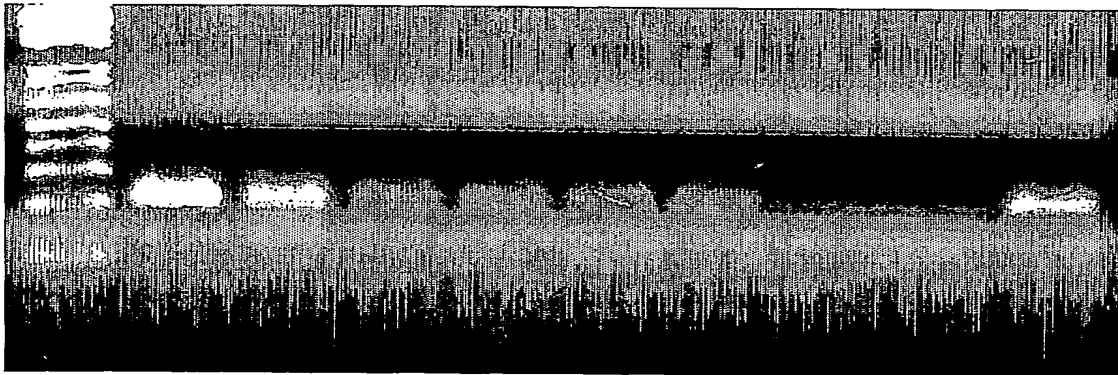
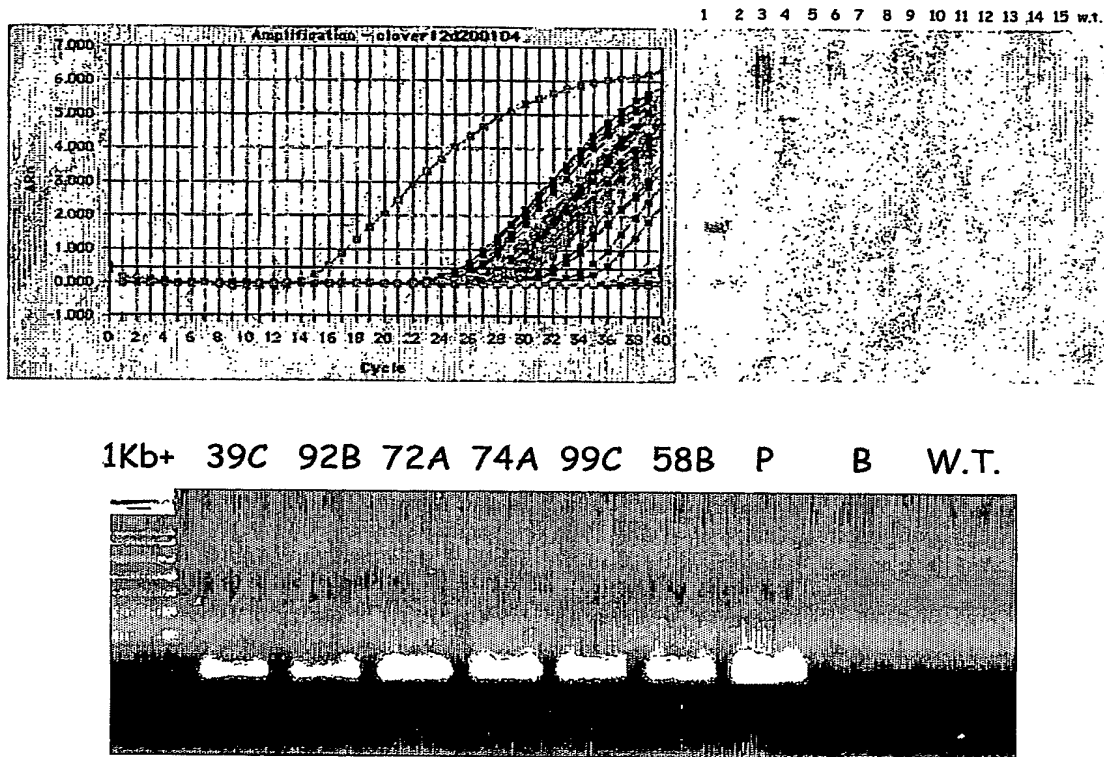


FIGURE 37

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1Kb+ 3A 22A 6B 24A 34A 29E Blank W.T. P

**FIGURE 38**

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